Example: K₂V₃O₈

Solution of (3+1)-dimensional incommensurately modulated structure with twinning from single crystal TOF Laue neutron diffraction data.

The average structure of $K_2V_3O_8$ is similar to that of fresnoite (<u>JANA2006_Cookbook</u> example 5.4)

Single crystal data were measured on the TOPAZ beamline at ORNL Spallation Neutron Source.

Input files: K2V3O8_Niggli.hkl, K2V3O8_Niggli.mat Data reduction and Absorption correction: done with software of the diffractometer

1. Creating new jobname

Start Jana2006

"File \rightarrow Structure \rightarrow New" opens a file manager Left pane: locate directory with input files Right pane: double-click K2V3O8_Niggli

2. Import Wizard

Select "Known diffractometer formats"; NEXT Select "TOPAZ"; NEXT [complete/correct experimental parameters] Change the temperature to 90; NEXT Leave all settings unchanged; NEXT The program reads 26335 reflections; OK; FINISH OK; YES to accept the data set CANCEL to cancel creating refinement reflection file

3. Symmetry Wizard

	Define/modify	y basic structural paramet	ers:	
Cell Symmetry Composition Multipole parameters Magnetic parameter				
Space group P1			Select from list	
Origin shift 0 0 0				
	The operators	s derived from the group symbo	si	
(1) v1 v2 v3 v4 v5	The operators	Load ->		
(1) 21 22 20 21 20			<- Add <- Rewrite	
		Delete	operator <u>C</u> lean out	
		Cell centeri	ng P 🔺	
			Complete the set	
			Make test	
		Rur	n Stokes & Campbell SSG-test	
		▼ Det	ine local symmetry operators	
		Esc Ok		

Double click EditM50 and select symmetry tab;

The lowest symmetry is use by default. The space group test for single TOF data is skipped in the symmetry wizard as each reflection can be considerably affected by extinction, which is dependent on the actual wave length. Then testing of Laue diffraction symmetry can fail. However, for space group tests based on systematic extinction can still be performed;

OK; Do not rewrite m50; Do not create reflection file; "File \rightarrow Reflection file \rightarrow Make space group test";

Define/modify ba	sic structural parameter	5:
Cell Symmetry Composition	Multipole parameters	Magnetic parameters
Tolerances for c	rystal system recognition	:
Original cell parameters: 8.901 8.881 5.195 90.0	02 90.02 90.02	4
Maximal deviation for cell lengths in [A] 0.03		
Maximal deviation for cell angles in deg 0.2		
Maximal deviation for modulation vector 0.01		-
Tolerances for	space group recognition:	
Maximal ave(I/sig(I)) for centering 5		
Maximal ave(I/sig(I)) for extinctions 10		
Search for higher symmetrical supercell (reco	ommended)	
Introduce twin laws in case of subgroups		
Use old twin matrices in testing		
2.4	((Court 1
Back	Next	Cancel
Es	c Ok	

Change "Maximal deviation for cell length in [A]" to 0.03; NEXT OK; select tetragonal 4/mmm; NEXT Default select P centering; NEXT Select P4bm; NEXT (Several space group symmetries are possible based on the extinction condition and Rint, need other information or several attempts to determine the correct space group symmetry. User can follow example 5.4 to determine the correct space group symmetry for average structure)

FINISH; OK and YES to accept changes

4. Creating refinement reflection file

YES to start the reflection wizard Follow default steps of the reflection wizard 91/175 reflections discarded due to space group symmetry (some of these reflections are quite strong, indicates the true symmetry might be lower, which will be dealt with later)

5. Solution of average structure

Start "Tools \rightarrow Transformation \rightarrow Go to average 3d structure" For name use "ave_P4bm" Follow the steps of the Reflection wizard

Continue with the new structure

Start "Run → Solution"

For Formula type "K V O"

Rub "Start solution" - rirth mouse double click on the icon;

Select "Superflip" and "Peaks from Jana2006"

Select "Use a specific random seed" and type "111" for random seed

With this option result of charge flipping will be the same in most computers and origin position and special atomic position will be equivalent with this cookbook. For normal work random seed should not be fixed.

OK

Superflip converges with R around 23% and confirms the selected space group Draw structure shows that all the peaks are assigned with oxygen atoms



The four atoms in one layer originated from equivalent positions of O5 atom should be the K atoms, and the V atoms are missing Accept the result Run "Edit atom" and change O5 to atom the type to K: OK Select all atoms; Action; Rename selected atoms to "atom_type" + number Use harmonic ADPs for all five atoms Draw structure shows the correct position of K atoms



Run Refinements on F(obs)**2 with number of cycles changed to at least 100, skip any warnings that might appear Refinement converges with Robs=7.03% Run difference Fourier with 0.01x0.01x0.005 resolution We need to find the position of the V atoms using the difference Fourier map Run Contour; New plot; Options - Fourier map, calculate new ones; draw maps as calculated

	Fourier co	ommands	
Basic	Scop	e	Peaks
Map type F(obs)-F(calc) - d	fference Fourier	T	U(iso)
\underline{O} mit not-matching reflections			
Use weighting of reflections	\checkmark		
Apply sin(th)/lambda limits			
		ma <u>x</u> .	
			Browse
	Esc	Ok	

	Fourier commands	
Basic	Scope	Peaks
automatically	explicitly	by a central point
0	۲	0
✓Use <u>d</u> efault map orienta	tion	
Map axes: 1st=horizo	ntal, 2nd=vertical, 3rd=section	l,
1st 2nd 3rd	minimum	maximum step
x	0	0.99 0.01
у	0	0.99 0.01
z	0	0.995 0.005
	Reset to default	
	Esc	

"Run 3d maps" to plot the difference map in 3D, set the isosurfaces level to 1.5 to show only strong peaks.

The large blue spheres are the negative peaks showing the position of V atoms.



Right click Fourier function and open peaks tab, change charge integration sphere radius to 0.3. (the neutron scatter off the nuclei of the atom, so the sphere radius is much smaller than the electron peak in X-ray diffraction)

	Fourier commands	
Basic	Scope	Peaks
search for peaks in the c	alculated map	
Maximum number of pea	ks:	
O Default		
Explicitly Positive	5 <u>N</u> egative	5
	Charge integratio	n:
 in a fixed sphere of radiu 	s => 0.3	
 in an adjusted shape with 	nin maximal radius	
The second method is mo	re precise but slower	
	Esc Ok	

Run Fourier and add difference minima Min1 and Min2 as V atoms.

The scattering length of V is negative, so the minimum peaks are what we should look for Right click refinement function;

Go to the page "Various" and press button "Fixed command";

Select "Origin" and fill the atom O2 used for fixing the origin in the polar space group P4bm; Go to the page "Basic" and modify the dumping factor to 0.2 and enlarge the number of refinement cycles to 100;

Run Refinement

Refinement converges with Robs=5.74% In EditM50 check formula: K2 V3 O8 with Z=2 Plot structure to see the final average structure. 2D V tetrahedra and pyramid net work separated by layers of K atoms.





6. Back to the modulated structure

"File → Structure → Open": open "K2V3O8_Niggli"
In EditM50 enter formula "K V O" in composition
"File → Structure → Copy in": import **only** M40 from the average structure "ave_P4bm"
Fix the origin in analogical way as for the average structure.
Run refinement on F(obs)**2.
Refinement confirms R value for the average structure:

```
 \begin{array}{ll} \mbox{R factors}: [26160 = 21667 + 4493/55], & \mbox{Damping factor}: & 1.0000 \\ \mbox{GOF(obs)} = & 5.71 & \mbox{GOF(all)} = & 5.30 \\ \mbox{R(obs)} = & 21.45 & \mbox{wR2(obs)} = & 36.55 & \mbox{R(all)} = & 24.43 & \mbox{wR2(all)} = & 37.18 \\ \mbox{R factors for main reflections}: & [10570 = 10298 + 272] \\ \mbox{R(obs)} = & 5.74 & \mbox{wR2(obs)} = & 13.63 & \mbox{R(all)} = & 5.92 & \mbox{wR2(all)} = & 13.69 \\ \mbox{R factors for satellites} + & (1,0): & [15590 = 11369 + 4221] \\ \mbox{R(obs)} = & 100.00 & \mbox{wR2(obs)} = & 100.00 & \mbox{R(all)} = & 100.00 \\ \mbox{Last wR2(all)}: \\ \mbox{Maximum change/s.u.}: & 0.0050 & \mbox{for y}[O3] \\ \end{array}
```

7. Superspace symmetry

The translation part of the superspace symmetry operators needs to be completed. Start EditM50

Go to page "Symmetry"

Focus the textbox "Space group" and press TAB.

The program offers the first symmetry operator needing to complete:



At the first attempt try combination 0 0 for the first operator and ½ 0 for the second one. The program will not allow it.

Unlike the case of Example 5.4, the number of discarded peaks due to the symmetry are about the same for the two different combinations 0 0 + 0 0 or $0 0 + \frac{1}{2}$ ½, due to the absence of second order satellite peaks or cross terms, which makes it not useful for determining the correct superspace group. Therefore, both cases need to be tried in the refinement and see which one works. And the same as fresnoite structure, $0 0 + \frac{1}{2}$ ½ turns out to be the correct combination.

For translation parts use combination 0 0 + $\frac{1}{2}$ $\frac{1}{2}$ Re-create refinement reflection file

Reflections I < Note: this num	3 *sig(I) will be sorted as unobserved ber is not interpreted by REFINE ut file E-format (recommended for data with large dynamical rar	nge)
	Import statistics - obs/all 21758/26335 reflections read from input file 21654/26093 reflections written to output file 104/242 reflections rejected as systematically extinct.	
	Back	Cancel

8. Refinement of modulated structure – position modulation

Make a copy for modulated structure: "mod_P4bm" to work with Make sure fix command "fixed origin O2" is present "Edit atoms": set two position modulation waves for all atoms This means one harmonic wave along the first wave vector (q1) and one harmonic wave along the second wave vector (q2) Run refinement Refinement converges with the following Robs values for all reflections, main reflections and 1st satellites: 6.9%, 5.73%, 12.75%

"Edit atoms": add two modulation waves for ADP 2nd on all atoms

Run refinement

Refinement converges with slightly better Robs values: 6.82%, 5.7%, 12.4%. There are warning for negative ADP for V atoms. This can be fixed by fixing the ADP to a reasonable positive value, which won't change the R values much.

9. Extinction correction



Select "Isotropic-Becker&Coppens" "Type 1" "Lorentzian" Change Radius [cm] to 0.1 and set the starting GIso to a smaller value, i.e. 0.0001; OK

	Extinction	model:			
None	0	Type <u>1</u>	•	<u>G</u> aussian 🔘	
Isotropic - Becker & Coppens	•	Type <u>2</u>	0	Lorentzian 💿	
Anisotropic - Becker & Coppens	0	<u>M</u> ixed	0		
SHELX model	0				
Radius [cm] 0.1	used only if the	ar not pre	sent on M90 file		
	Extinction pa	aramete	rs:		
GIso 0.0001					
Refine all Fix all Reset					
	Esc	Ok]		

Double-click Refine and refine the structure

Refinement converges with slightly better Robs values: 6.18%, 4.96%, 12.28%. Check the extinction coefficient through "Parameters \rightarrow Extinction"

	Extinction	model:		
None	0	Type <u>1</u>	\odot	Gaussian 🔘
Isotropic - Becker & Coppens	\odot	Type 2	0	Lorentzian 💿
Anisotropic - Becker & Coppens	0	<u>M</u> ixed	0	
SHELX_model	0			
Radius [cm] 0.1	used only if tba	r not pre	sent on M90 file	
	Extinction pa	ramete	rs:	
GIso 0.003282				
Refine	all <u>F</u> ix a		Reset	
	Esc	Ok		

Plot a 5x5x1 *super structure. Each individual V polyhedron is not distorted, the framework is modulated by changing the angles between the polyhedra.*



10. Reimport data and create merged refinement reflection file

Make new copy for modulated structure: "mod_P4bm_merged" to work with "File \rightarrow Reflection file \rightarrow Import/modify the reflection file":

File Edit/View Run Wizards Parameters Tools Start shell Export structure to • <t< th=""><th>Jana2</th><th>2006</th><th></th><th></th><th></th><th></th><th></th><th></th><th></th></t<>	Jana2	2006							
Start shell Export structure to QIF utilities Structure Import model from Reflection file Import/modify the reflection file Cyclic refinement Make space group test Create refinement reflection file Handle culling manually File Type Radiation K2V3O8_Niggli.hkl Info Reimport Modify Delete	File	Edit/View	Run	<u>W</u> izards	Parameters	Tools			
Export structure to • CIF utilities • Structure • Import model from • Reflection file • Cyclic refinement • Exit • Greate refinement reflection file Handle culling manually Pata repository File Type Radiation K2V3O8_Niggli.hkl [Single crystal Info Reimport Modify Delete	Start s	shell							
GIF utilities • Structure • Import model from • Reflection file • Cyclic refinement • Make space group test • Create refinement reflection file • Handle culling manually • File Type Radiation K2V3O8_Niggli.hkl [Single crystal Info Reimport Madify Delete	Export	t structure to	►						
Structure Import model from Import model from Import/modify the reflection file Reflection file Import/modify the reflection file Cyclic refinement Make space group test Exit Greate refinement reflection file Handle culling manually Handle culling manually Data repository File Type K2V3O8_Niggli.hkl [Single crystal Info Reimport Modify Delete	<u>C</u> IF ut	ilities	►						
Import model from Import/modify the reflection file Reflection file Import/modify the reflection file Cyclic refinement Make space group test Exit Create refinement reflection file Handle culling manually Data repository File Type Radiation K2v3O8_Niggli.hkl [Single crystal [Neutrons TOF	Struct	ure	•						
Reflection file Import/modify the reflection file Cyclic refinement Make space group test Create refinement reflection file Handle culling manually Data repository File Type Radiation K2V3O8_Niggli.hkl Single crystal Neutrons TOF	Import	t model from	•						
Cyclic refinement Make space group test Exit Greate refinement reflection file Handle culling manually Handle culling manually Data repository File Type Radiation K2V308_Niggli.hkl Isingle crystal INeutrons TOF	Reflec	tion file	Þ	Import/modi	fy the reflection	n file			
Exit Create refinement reflection file Handle culling manually Data repository File Type Radiation K2V3O8_Niggli.hkl [Single crystal Info Reimport	Cyclic	refinement	Þ	Make space	group test				
Handle culling manually Data repository File Type Radiation K2V308_Niggli.hkl I Single crystal I Neutrons TOF	Exit			Create refin	ement reflectio	on file			
Data repository File Type Radiation K2V308_Niggli.hkl [Single crystal [Neutrons TOF				Handle cullin	ig manually				
Data repository File Type Radiation K2V308_Niggli.hkl ISingle crystal INeutrons TOF									
File Type Radiation K2V3O8_Niggli.hkl Single crystal Neutrons TOF					Data	reposite	ory		
K2V3O8_Niggli.hkl Single crystal Neutrons TOF Info Reimport Modify Delete Location	File					Туре		Radiat	tion
Info Reimport Modify Delete Dedelato Import peur	K2V3C	08_Niggli.hkl				Single	crystal	Neutro	ns TOF
Info Reimport Modify Delete Uddelato Import pew									
Info Reimport Modify Delete Decesion Import peur									
Info Reimport Modify Delete Hadelata Import new									
		Info		Reimport	Modify		Delete	Undelete	Import new

IMPORT NEW

Select "reflection file corrected for LP and absorption"; NEXT

Select "General file on I", enter file name "K2V3O8_Niggli.hkl", change Input format to (6i4,2f8.2); NEXT

Esc

Ok

*

Ŧ

		Single crystal dat	a from:	
File name	K2V3O8_Niggli.hkl			Browse
O SHEL	X on F	0	From FullProf file	
O SHEL	X on I	0	From XD file	
O SHEL	X HKLE5	0	From DABEX	
O IPDS	STOE	0	Jana2006-M90	
O CCD	Bruker	0	General file on F	
O From	<u>C</u> IF file	۲	General file on I	
O From	Graindex file			
Input forma	at: (6i4,2f8.2)			
			(
		Back	Next	Cancel

Select Neutrons and o	change Wave	length to 0.4; N	NEXT Leave all s	settings unchanged; NEXT
-----------------------	-------------	------------------	------------------	--------------------------

	Complete/correct experimental parameters	
Cell parameters:	8.8911 8.8911 5.1949 90 90 90	
Number of input indices:	6 Info about metrics parameters	
1st modulation vector:		
2nd modulation vector:		
3rd modulation vector:		
○ <u>X</u> -rays		
 Neutrons 		
○ Electrons		
Wave length 0.4		
Temperature 90		
	Badk Next	Cancel

OK to continue with the old ones

Relationship to the reference cell/split by twinning						
Cell parameters: 8.8911 8.8911 5.1949 90.000 90.000 90.000						
Target dimension: 5						
1st modulation vector 0.3145 0.3145 0.5000	Number of domains : 1					
2nd modulation vector -0.3145 0.3145 0.5000	Data related to domain#					
	Multiply input F(hkl)/I(hkl) by 1					
Max. satellite index	Import only satellites					
Accuracy Define transform S.U. of original cell parameters differs free Octinue Continue with the old ones Use the new ones Ok	om those just importerd,					
Back	Cancel					

The program reads 26335 reflections; OK; FINISH

Delete the original data by clicking DELETE

			Data repository		
File			Туре	Radiation	
K2V3O8	_Niggli.hkl		Single crystal	Neutrons TOF	
K2V3O8	3_Niggli.hkl		I (hkl) imported	Neutrons 0.4	
	Info	Reimport	Modify Delete	Undelete Import new	
			Esc Ok		
			Data repository		
File			Data repository Type	Radiation	
File K2V3O8	3_Niggli.hkl		Data repository Type Deleted	Radiation	
File K2V308 K2V308	3_Niggli.hkl 3_Niggli.hkl		Data repository Type Deleted I(hkl) imported	Radiation	
File K2V3O8 K2V3O8	3_Niggli.hkl 3_Niggli.hkl		Data repository Type Deleted I (hkl) imported	Radiation	
File K2V308 K2V308	3_Niggli.hkl 3_Niggli.hkl		Data repository Type Deleted I(hkl) imported	Radiation	
File K2V308 K2V308	Niggli.hkl Niggli.hkl Info	Reimport	Data repository Type Deleted [I(hkl) imported Modify	Radiation Neutrons 0.4 Undelete Import new	▲
File K2V308 K2V308	3_Niggli.hkl 8_Niggli.hkl Info	<u>R</u> eimport	Data repository Type Deleted [I(hkl) imported] Modify Delete Esc Ok	Radiation Neutrons 0.4 Undelete Import new	▲

Highlight the newly imported data and OK; YES to accept the data set Follow default steps of the reflection wizard

The program discards 242 reflections, 110 observed, Rint=10.23%. This newly imported data merged 21654/26093 reflections to 5488/6034 reflections, which would expedite the refinement process by a lot.

"Parameters \rightarrow Scale":

Jana	2006				
<u>F</u> ile	Edit/View	<u>R</u> un	<u>W</u> izards	<u>P</u> arameters	<u>T</u> ools
				Options	
				Scale	
				Twin fractions	
				Extinction	
				<u>f</u> ,f	
				Powder	
				<u>A</u> toms	•
				Molecules	•
				Electron diffra	ction

Change Maximal number of scales to "6"

	Edit scale parameters									
TOverall	이		sclam/2							
	<u>M</u> aximal nu	mber (of scales	23 🚔						
scale 1	2.285593	\checkmark	scale2	2.214194		scale3	2.140421	\checkmark		
scale4	2.204709	\checkmark	scale5	2.188174	\checkmark	scale6	2.293736	\checkmark		
scale7	2.210344	\checkmark	scale8	2.153546		scale9	2.128025			
scale 10	2.308868	\mathbf{V}	scale 11	2.067626		scale 12	2.151474			
scale 13	2.234085	\mathbf{V}	scale 14	2.218911	\mathbf{V}	scale 15	2.081075			
scale 16	2.187914	\mathbf{V}	scale 17	2.113101	\mathbf{V}	scale 18	2.204085			
scale 19	2.202408	\mathbf{V}	scale20	2.124971		scale21	1.933063			
scale22	2.232141	\checkmark	scale23	2.087145	\mathbf{V}					
Refine all Fix all										
			Esc	Ok						

Change all the scales to "0" except scale1, and fix all except scale1 for refinement.

Edit scale parameters	
TOverall 0 sclam/2	sc3lam
Maximal number of scales	
scale4 0 scale5 0	scale6
<u>R</u> efine all <u>Fix all</u>	
Esc Ok	

Double-click Refine and refine the structure Refinement converges with Robs values: 6.30%, 3.72%, 13.40%.

R factors : [6034=5573+461/123], Damping factor: 1.0000								
GOF(obs)= 2.21 (GOF(all)= 2.16							
R(obs)= 6.30 v	wR2(obs)= 11.18	R(all)= 6.85	wR2(all)= 11.37					
R factors for main re	eflections : [1798=17	783+15]						
R(obs)= 3.72 v	wR2(obs)= 8.07	R(all)= 3.79	wR2(all)= 8.09					
R factors for satellite	R factors for satellites +-(1,0) : [4236=3790+446]							
R(obs)= 13.40 v	wR2(obs)= 19.94	R(all)= 14.64	wR2(all)= 20.45					
Last wR2(all): 11.37								
Maximum change/s.u. : 0.0182 for xsin1[O2]								

In most cases where the instrument is well-calibrated, the refinement result should be similar for the merged and unmerged data. However, the extinction correction is dependent on the wavelength which is different for peaks collected from different runs, and merging data from different runs would erase that information. Therefore, the unmerged data is recommended for publication especially for crystals with strong extinction.

11. Refinement of modulated structure with subgroup symmetry "Tools \rightarrow Transformations \rightarrow Go to subgroup structure":

Jana:	2006							
File	Edit/View	Run	<u>W</u> izards	Parameters	Tools			
					Recover	r files		
					Transfo	rmations	Þ	Cell transformation
					Special	tools	Þ	Change modulation vector
					Powder		Þ	Origin shift
					Phases		•	Change enantiomorph
					Charge		Þ	Go to subgroup structure
					Tools fo		Þ	Go to supercell structure
					Graphic		⊧	Go to average <u>3</u> d structure
					Recipro	cal space viewer		Transform to the supercentered cell
					Files for	MEM	Þ	Transform from amplimodes
					Prefere	nces		
					Program	IS		
					Connect	t through internet to	۲	
					About J	ana2006		

SELECT NON-ISOMORPHIC SUBGROUP; select Cmm2

The discarded peaks are mostly violating the extinction condition of the b-glide plane, so P4 and Cmm2. The average structure shows clear P4bm symmetry, with all the mirror planes present, and the most probable way to break the symmetry is the modulation happens along only one direction, instead of 2. (3+1)d structure for tetragonal structure is only possible when the modulation is along c-axis, which obviously isn't the case in this structure. Therefore, the most probable symmetry is orthorhombic Cmm2.



OK; NEXT; NEXT select the default operator; NEXT

Name the structure "mod_Cmm2_merged"; leave the Make as twinned structure box checked

The program will automatically create twin domains with equal volume and have the twin matrix applied.

NEXT; FINISH

Follow default steps of the reflection wizard

Only 16/67 reflections are rejected as systematically extinct for the new space group, all of them are really weak peaks.

Don't apply the transformation at the end; NO



You can transform to the standard setting anytime you want, keep the structure in the primitive setting would allow easy reimportation of the data if you want to refine the structure against the unmerged data

YES to continue with the new structure

Open Edit atoms, SELECT ALL to edit/define atoms

There are 12 atoms now, all but O2 and V2 are duplicated to two sites from the tetragonal structure.

Reduce the number of modulation waves to 1 for both position and ADP 2nd.

Step	#1: Select atoms to be used -> 12	selected	
01		Atom e	edit
01	D	efine	Edit
02	Type		
03	ADP parameter(s):	Modulation waves:	
04	🔘 įsotropic	Occupancy 0	Use: crenel
04	O <u>h</u> armonic (anisotropic)	Position 1	Use: saw-tooth zig-zag
K1 K1	O anharmonic	ADP 2nd 1	Type of modulation functions:
V1	O Use TLS		O harmonics (0,1)
۷1			harmonics (0, 1) orthogonalized to crenel interval
┛			C Legendre polynomials in crenel interval
			x-harmonics in crenel interval
			Selection limit for harmonics:
Ster			
		Esc	Ok
		ESC	UK

OK; OK; YES to accept changes

We came from superspace group P4bm($\alpha,\alpha,\frac{1}{2}$)(- $\alpha,\alpha,\frac{1}{2}$)0gg to Cmm2($\beta,0,\frac{1}{2}$)0s0($\beta,\frac{1}{2},0$)00s, which is still a (3+2) dimensional superspace group. This is necessary because the data imported is in the form of a (3+2) dimensional structure, even though it could be a (3+1)d structure with 90 degree twinning. By reducing the number of modulation waves to 1, we are only allowing the modulating along one direction to happen, which effectively makes the symmetry to be Cmm2($\beta,0,\frac{1}{2}$)0s0, which is a (3+1)d group. This works pretty easily in this case because only first order satellite peaks are observed in the diffraction pattern. If higher order satellite peaks are observed, we would need to define the 3rd, 4th and higher order modulation waves, and add fix commands to fix all the even order modulation waves to be zero.

Change the damping factor to 0.5 and start to refine the structure

Refinement converges with Robs values: 6.54%, 4.39%, 13.13%, 12.99%. It may take a long time to reach the convergence criteria, you can end the refinement early when it gets close.

R factors : [9118=	=8175+943/153], Da	mping factor: 0	.2000			
GOF(obs)= 2.22	GOF(all) = 2.15					
Number of reflecti	ons excluded due to re	finement options	:0+0			
R(obs)= 6.53	wR2(obs)= 12.15	R(all)= 7.15	wR2(all)=	12.40		
R factors for main	reflections : [2920=28	350+70]				
R(obs)= 4.39	wR2(obs)= 9.47	R(all)= 4.53	wR2(all)=	9.52		
R factors for satel	lites +-(1,0) : [3192=2	2767+425]				
R(obs)= 13.13	wR2(obs)= 21.24	R(all)= 14.26	wR2(all)=	21.80		
R factors for satel	lites +-(0,1) : [3006=2	2558+448]				
R(obs)= 12.99	wR2(obs)= 21.48	R(all)= 14.41	wR2(all)=	22.27		
Last wR2(all): 12.40 12.40 12.40 12.40 12.40 12.40 12.40 12.40						
Maximum change/s.u. : -1.7353 for z[V2]						

[&]quot;Parameters \rightarrow Twin fractions"; REFINE ALL; OK; YES to accept changes

🤳 Jana	2006				
File	Edit/View	<u>R</u> un	<u>W</u> izards	<u>P</u> arameters	Tools
				Options	
				<u>S</u> cale	
				Twin fractions	
				Extinction	
				<u>f</u> ,f"	
				Powder	
				<u>A</u> toms	•
				Molecules	•
				Electron diffra	ction

Double-click Refine and refine the structure with twin fractions turned on *Refinement converges with Robs values: 6.47%, 4.38%, 12.56%, 13.09%. The resulting twin fraction is 0.472126.*





Because the structure is in non-standard setting for space group Cmm2, there is no entry in the space group box, only the symmetry operation listed. We can now reimport the hkl file

as TOPAZ format to refine the structure against the unmerged reflection file, following **Reimport data and create merged refinement reflection file** steps, the program will automatically adjust the number of scale factors this time.

Cell Symmetry Composition Multipole parameters Magnetic parameters Space group	Define/mo	dify basic structural param	neters:
Space group Qrigin shift (1) x1 x2 x3 x4 x5 (2) -x1 +x2 x3 x3 x4 x3 x5 (3) -x2 +1/2 x1 +1/2 x3 x3 x4 +1/2 x5 +1/2 (4) x2 +1/2 x1 +1/2 x3 x4 +1/2 x3 -x5 +1/2 (4) x2 +1/2 x1 +1/2 x3 x4 +1/2 x3 -x5 +1/2 (cell centering Complete the set Make test Make test Run Stokes & Campbell SSG-test Define local symmetry operators	Cell Symmetry Composition	Multipole parameters	Magnetic parameters
(1) x1 x2 x3 x4x5 (2) -x1 -x2 x3 x3-x4 x3-x5 (3) -x2+1/2 -x1+1/2 x3 x3-x4+1/2 x5+1/2 (4) x2+1/2 x1+1/2 x3 x4+1/2 x3-x5+1/2 (4) x2+1/2 x1+1/2 x3 x4+1/2 x3-x5+1/2 (4) x2+1/2 x1+1/2 x3 x4+1/2 x3-x5+1/2 (5) Cell centering (6) Complete the set (7) Make test (8) Make test (9) Define local symmetry operators	Space group]	Select from list
	(1) x1 x2 x3 x4 x5 (2) -x1 -x2 x3 x3 x4 x3 x5 (3) -x2+1/2 -x1+1/2 x3 x3 -x4+1/2 x5+1/2 (4) x2+1/2 x1+1/2 x3 x4+1/2 x3 -x5+1/2	Load ->	Complete the set Make test Make test
			Define local symmetry operators

12. Transform the structure to standard orthorhombic setting

🤳 Jana2	2006							
File	Edit/View	Run	<u>W</u> izards	Parameters	Tools			
					Recover	r files		
					Transfo	rmations	Þ	Cell transformation
					Special t	tools	Þ	Change modulation vector
								Origin shift
					Phases		Þ	Change enantiomorph
								Go to subgroup structure
								Go to supercell structure
					Graphic		Þ	Go to average <u>3</u> d structure
					Recipro	cal space viewer		Transform to the supercentered cell
					Files for	MEM	Þ	Transform from amplimodes
					Preferen	nces		
					Program	IS		
					Connect	t through internet to	Þ	
					About J	ana2006		

"Tools \rightarrow Transformations \rightarrow Cell transformation":

Click BY A MATRIX, enter the transformation matrix shown when we created the subgroup structure.



Transformed cell parameters - Volume						
12.5739 12.5739 5.1949 90.000 90.000 90.000 821.3 <u>B</u> ack						
Cumulative matrix						
a'= -1.000*a -1.000*b +0.000*c						
b'= -1.000*a +1.000*b +0.000*c						
c'= 0.000*a +0.000*b -1.000*c Eorward						
Transform:						
to the <u>r</u> educed cell	to the reduced cell to those from data collection					
to a <u>d</u> ouble cell	by a <u>m</u> atrix					
matri <u>x</u> calculator	by a special matrix					
Esc Ok						

OK to rewrite the old structure. Follow default steps of the reflection wizard Open EditM50 and the symmetry tab The space group box correctly displays Cmm2 with origin shift $\frac{1}{4}$ $\frac{1}{4}$ 0 "Tools \rightarrow Transformations \rightarrow Origin shift":

Jana2	2006							
File	Edit/View	<u>R</u> un	<u>W</u> izards	Parameters	Tools			
					Recover files			
					Transformations		Þ	Cell transformation
					Special tools		Þ	Change modulation vector
								<u>O</u> rigin shift
					Phases		Þ	Change enantiomorph
								Go to subgroup structure
								Go to supercell structure
					Graphic	:	•	Go to average <u>3</u> d structure
					Recipro	cal space viewer		Transform to the supercentered cell
					Files for	r M <u>E</u> M	Þ	Transform from amplimodes
					Prefere	nces		
					Program	ns		
					Connec	t through internet to	Þ	
					About 1	Jana2006		

Enter 0.25 for x1 and x2

Move the origin to:								
• Point:	x1 0.25 x2 0.25 x3 0 x4 0 x5 0							
O Atom:								
	Ok							

ОК

"Tools \rightarrow Transformations \rightarrow Change modulation vector":

🥕 Jana2006



The modulation vectors have negative values now, it's better to change them to positive values.

 $q1'=(0\ 0\ 0) + (-1)*q1 + (0)*q2$ $q2'=(0\ 0\ 1) + (0)*q1 + (1)*q2$ and click the upward arrow

Original modulation vectors		Transformed modulation vectors			
q1:-0.6289 0.0000 -0.5 q2: 0.0000 0.6289 -0.5	000 000	q1': 0.6289 0.0000 0.5000 q2': 0.0000 0.6289 0.5000			
q1'=	000	+ -1	*q1+ 0	*q2	
q2'=	001	+ 0	*q1+ 1	*q2	
Ok					

Now the transformed modulation vectors are all positive values OK; OK to rewrite the old structure Follow default steps of the reflection wizard

The structure is in standard setting of the space group symmetry now. Double-click Refine and refine the structure

If you are refining against the unmerged data set imported in TOPAZ format, the refinement eventually converges with Robs values: 6.15%, 4.98%, 11.95%, 12.05%.

```
R factors : [26268=21745+4523/176], Damping factor: 0.1000
GOF(obs) = 1.98 GOF(all) = 1.88
Number of reflections excluded due to refinement options: 0+0
                wR2(obs)= 12.64
                                     R(all) = 6.86
                                                     wR2(all)= 13.17
R(obs) = 6.15
R factors for main reflections : [10745=10389+356]
R(obs) = 4.98
                wR2(obs)= 10.66
                                     R(all) = 5.18
                                                    wR2(all) = 10.76
R factors for satellites +-(1,0) : [8050=5961+2089]
R(obs)= 11.95
                wR2(obs)= 22.55
                                     R(all) = 13.62
                                                     wR2(all)= 24.20
R factors for satellites +-(0,1) : [7473=5395+2078]
               wR2(obs)= 22.45
                                     R(all)= 13.93
                                                     wR2(all)= 24.44
R(obs) = 12.05
Last wR2(all): 13.18
Maximum change/s.u. : -4.7513 for z[V2]
```

Plot a 5x1x1 super structure. This structure only have modulation along a-axis and is periodic along b and c-axis.

